

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/540,615
Source: PCT
Date Processed by STIC: 07-11-2005

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/540,615

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). ~~<220>-<223> section is required when <213> response is Unknown or is Artificial Sequence~~

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



PCT

RAW SEQUENCE LISTING

DATE: 07/11/2005

PATENT APPLICATION: US/10/540,615

TIME: 15:15:15

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\07112005\J540615.raw

4 <110> APPLICANT: CENTER FOR GENETIC ENGINEERING AND BIOTECHNOLOGY
 6 <120> TITLE OF INVENTION: RECOMBINANT HEPATITIS A VIRUS ANTIGENS PRODUCED IN PLANT CELLS.
 9 <130> FILE REFERENCE: ORF.
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/540,615
 C--> 12 <141> CURRENT FILING DATE: 2005-06-23
 14 <160> NUMBER OF SEQ ID NOS: 24
 16 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 25
 E--> 20 <212> TYPE: ADN *ADN* *Does Not Comply*
 21 <213> ORGANISM: Chimeric Sequence *Corrected Diskette Needed*
 24 <220> FEATURE: *Invalid*
 25 <221> NAME/KEY: primer_bind *Response see item # 10 on*
 26 <222> LOCATION: (1)..(25) *error summary sheet.*
 27 <223> OTHER INFORMATION: Sequence # 1.
 28 Sequence of the oligonucleotide # 1 used for the amplification of ORF
 29 coding sequence by RT-PCR.
 32 <400> SEQUENCE: 1
 33 cttaatatctag aatgaatatg tccaa 25
 36 <210> SEQ ID NO: 2
 37 <211> LENGTH: 22
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 39 <213> ORGANISM: Chimeric Sequence *Same error*
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 42 <221> NAME/KEY: primer_bind
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 44 <223> OTHER INFORMATION: Sequence # 2.
 45 Sequence of the oligonucleotide # 2 used for the amplification of ORF
 46 coding sequence by RT-PCR.
 47 <400> SEQUENCE: 2
 48 gaaagaaata aaggtacctc ag 22
 51 <210> SEQ ID NO: 3
 52 <211> LENGTH: 6685
 E--> 53 <212> TYPE: ADN *Same error*
 54 <213> ORGANISM: Hepatitis A virus
 56 <220> FEATURE:
 57 <221> NAME/KEY: gene
 58 <222> LOCATION: Complement((1)..(6685))
 59 <223> OTHER INFORMATION: Sequence # 3.

RAW SEQUENCE LISTING

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60 Nucleotide sequence coding for the HAV open reading frame (ORF) of the
 61 Cuban M2 strain.

64 <400> SEQUENCE: 3

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65 atgaatatgt ccaaacaagg aattttccag actgttggga gtggccttga ccacatcctg 60
66 tccttggcag atattgagga agagcaaattg attcagtcctg ttgataggac tgcagtgact 120
67 ggagcttctt atttcacttc tgtggaccaa tcttcagttc atactgctga ggttggctca 180
68 caccaaattg aacctttgaa aacctctgtt gataaacctg gttctaagaa aactcagggg 240
69 gagaagtttt tcttgattca ttctgctgat tggctcacta cacatgctct ctttcatgaa 300
70 gttgcaaaat tggatgtggt gaaactgctg tacaatgagc agtttgccgt ccaagggtttg 360
71 ttgagatacc atacttatgc aagatttggc attgagattc aagttcagat aaatcccaca 420
72 ccctttcagc aaggaggact aatctgtgcc atggttcctg gtgaccaaag ttatggttca 480
73 atagcatcct tgactgttta tcctcatggt ctgttaaatt gcaatatcaa caatgtagtt 540
74 agaataaagg ttccatttat ttatactaga ggtgcttctc attttaaaga tccacagtac 600
75 ccagtttggg aattgacaat cagagtttgg tcagagtga atattggaac aggaacctca 660
76 gcttatactt cactcaatgt tttagctagg ttacagatt tggagtgtga tggattaact 720
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91 gatttaaaag ggaaagccaa taggggaaag atggatgtat caggagtga ggtacctgtg 1620
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94 ggaaggcttc atttcttgtg tacttttact tttaattcaa acaataaaga gtacacattt 1800
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97 gccactgatg tggatggtat ggcctggttt actccagtgg gccttgctgt cgacaccctc 1980
98 tgggtggaaa agaagtcagc tttgtctatt gattataaaa ctgcccttgg agctgttaga 2040
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Output Set: N:\CRF4\07112005\J540615.raw

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112 gattttccaa atatgtctga gacagatttg tgtttcctgt tgcattggct aaatccaaag 2880
113 aaaattaatt tagcagatag aatgcttgga ttgtctggag tgcaggaaat taaagaacag 2940
114 ggtgttggac tgatagcaga gtgtagaact ttcttgatt ctattgctgg gactttgaaa 3000
115 tctatgattt ttgggtttca ttattctgtg actgttgaaa ttataaatat tgtgctttgt 3060
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117 cacataattg gtttgttgag agttatgaat tatgcagata ttggctgttc agtcatttca 3180
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121 tatgaagtaa attatggcaa gaaaaaggat gttcttaata ttctcaaaga taaccagcaa 3420
122 aaaatagaaa aagccattga agaagcagac aatttttgca ttttgcaaag tcaagatgtg 3480
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Output Set: N:\CRF4\07112005\J540615.raw

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163 gatagacagt gggatgaatt atttaaaaca atgataagat ttggagatgt tggctctgat 5940
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175 gagatgatat aatatagact taaatcttat gattgggtgga gaatgagatt ttatgaccag 6660
176 tgtttcattt gtgacctttc atgat 6685

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E--> 179 <210> SEQ ID NO: 4

180 <211> LENGTH: 40

E--> 181 <212> TYPE: **ADN** ← *p/s use type DNA*

182 <213> ORGANISM: Chimeric Sequence ← *same error*

184 <220> FEATURE:

185 <221> NAME/KEY: primer_bind

186 <222> LOCATION: (1)..(40)

187 <223> OTHER INFORMATION: Sequence # 4.

188 Sequence of the oligonucleotide # 5 used for the

189 amplification of P1-2A coding sequence by PCR.

192 <400> SEQUENCE: 4

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193 ttgaattcag cttgtgaaaa taacccttct attttcctag 40

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196 <210> SEQ ID NO: 5

197 <211> LENGTH: 28

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199 <213> ORGANISM: Chimeric Sequence

201 <220> FEATURE:

202 <221> NAME/KEY: primer_bind

203 <222> LOCATION: (1)..(28)

204 <223> OTHER INFORMATION: Sequence # 5.

206 Sequence of the oligonucleotide # 5 used for the

207 amplification of P1-2A coding sequence by PCR.

209 <400> SEQUENCE: 5

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210 cgcccggtc tagaatgaat atgtccaa 28

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213 <210> SEQ ID NO: 6

214 <211> LENGTH: 2523

E--> 215 <212> TYPE: **ADN** ← *same error*

216 <213> ORGANISM: Hepatitis A virus

218 <220> FEATURE:

219 <221> NAME/KEY: gene

220 <222> LOCATION: Complement((1)..(2523))

221 <223> OTHER INFORMATION: Sequence # 6.

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Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\07112005\J540615.raw

222 Nucleotide sequence coding for the structural
 223 P1-2A HAV proteins of the M2 strain.
 226 <400> SEQUENCE: 6
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 229 ggagcttctt atttcacttc tgtggaccaaa tcttcagttc atactgctga ggttggctca 180
 230 caccaaaattg aacctttgaa aacctctgtt gataaacctg gttctaagaa aactcagggg 240
 231 gagaagtttt tcttgattca ttctgctgat tggctcacta cacatgctct ctttcatgaa 300
 232 gttgcaaaat tggatgtggt gaaactgctg tacaatgagc agtttgccgt ccaaggtttg 360
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 237 ccagtttggg aattgacaat cagagtttgg tcagagttga atattggaac aggaacctca 660
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 250 gttgcttctc atgttagagt taatgtttat ctttcagcaa ttaatttgga atgttttgc 1440
 251 cctctttacc atgctatgga tgttaccaca caggttggag atgattcagg aggttttctca 1500
 252 acaacagttt ctacagagca gaatgttcct gatccccaag ttggcataac aaccatgagg 1560
 253 gattttaaag ggaaagccaa taggggaaag atggatgtat caggagtgca ggtacctgtg 1620
 254 ggagctatta caacaattga ggatccagtt ttagcaaaga aagtacctga gacatttcct 1680
 255 gaattgaagc ctggagaatc cagacataca tcagatcaca tgtctattta taaattcatg 1740
 256 ggaaggtctc atttcttgtg tacttttact tttaattcaa acaataaaga gtacacattt 1800
 257 ccaataactc tgtcttcgac ttctaactct cctcatgggt taccatcaac attaaggtgg 1860
 258 ttctttaatt tgtttcagtt gtatagagga ccattggatt tgacaattat aatcacagga 1920
 259 gccactgatg tggatggtat ggcctggttt actccagtgg gccttgctgt cgacaccctt 1980
 260 tgggtggaaa agaagtcagc tttgtctatt gattataaaa ctgcccttgg agctgttaga 2040
 261 tttaatacaa gaagaacagg gaacattcag attagattgc catggatttc ttatttgtat 2100
 262 gccgtgtctg gagcactgga tggcttggga gataagacag attctacatt tggattgggt 2160
 263 tctattcaga ttgcaaatca caatcattct gatgaatatt tgtccttttag ttgttatttg 2220
 264 tctgtcacag agcaatcaga gttctatttc cctagagctc cattaaattc aaatgctatg 2280
 265 ttgtccactg agtccatgat gagtagaatt gcagctggag acttggagtc atcagtggat 2340
 266 gatcccagat cagaggagga cagaagattt gagagtcata tagaatgtag gaaaccatat 2400
 267 aaagaattga gactggaggt tgggaaacaa agaatcaaat atgctcagga agagttatca 2460
 268 aatgaagtgc ttccacctcc taggaaaatg aaggggttat atgcttctgg aggtgaattc 2520
 269 gat 2523
 272 <210> SEQ ID NO: 7
 273 <211> LENGTH: 27
 E--> 274 <212> TYPE: ADM *Same error*

VERIFICATION SUMMARY

DATE: 07/11/2005

PATENT APPLICATION: US/10/540,615

TIME: 15:15:16

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\07112005\J540615.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:20 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:38 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:53 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:181 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:198 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:215 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:274 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:291 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:308 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:328 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:348 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:365 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:382 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:416 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:492 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:508 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:525 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:535 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:600 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:617 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:633 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:637 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
L:650 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:654 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21
L:667 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:726 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:759 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/540,615

DATE: 07/11/2005
TIME: 15:15:15

Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\07112005\J540615.raw

632 <211> LENGTH: 55
E--> 633 <212> TYPE: ADN ← Same error
634 <213> ORGANISM: Chimeric Sequence
636 <220> FEATURE:
W--> 637 <221> NAME/KEY: D_segment
638 <222> LOCATION: (1)..(54)
639 <223> OTHER INFORMATION: Sequence # 20
640 synthetic fragment modifying the 3' end of
641 the 2A protein and introduces a space-bar
642 between this one and the KDEL signal.
644 <400> SEQUENCE: 20
645 cctaggaaaa tgaagggggtt atatgcttct ggaggtgaat tcgatatcaa ggatg 55

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

RAW SEQUENCE LISTING

DATE: 07/11/2005

PATENT APPLICATION: US/10/540,615

TIME: 15:15:15

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\07112005\J540615.raw

```

573 attcagattg caaattacaa tcattctgat gaatatttgt ccttttagttg ttatttgtct 2160
574 gtcacagagc aatcagagtt ctatttcctt agagctccat taaattcaaa tgctatgttg 2220
575 tccactgagt ccatgatgag tagaattgca gctggagact tggagtcac agtggatgat 2280
576 ccagatcag aggaggacag aagatttgag agtcatatag aatgtaggaa accatataaa 2340
577 gaattgagac tggaggttg gaaacaaaga atcaaatatg ctgaggaaga gttatcaaat 2400
578 gaagtgcctt cacctcctag gaaaatgaag gggttatttt cacaagctga attcctgcag 2460
579 cccgggggat ccatgggaat ttcagatgat gacaatgata gtgcagtagc tgagtttttc 2520
580 cggctctttt catctggtga accatcaaat tccaagttat ctagtttttt ccaagctgtc 2580
581 actaatcaca agtgggttg tgtgggagct gcagttggta ttcttggatt gctagtggga 2640
582 ggatggtttg tgtataagca tttttccgc aaagaggaag aaccaattcc agctgttggg 2700
583 gtttatcatg gagtgactaa gcccaaaca gtgattaaat tggatgcaga tccagtagag 2760
584 tctcagttga ctctagaaat agcaggatta gtaggaaaa atttggttca gtttggagtt 2820
585 ggtgagaaaa atggatgtgt gagatgggtc atgaatgcct taggagtga ggtgattgg 2880
586 ttgttagtac ctctcatgc ttataaaatt gaaaaggatt atgaaatgat ggagttttat 2940
587 ttcaatagag gtggaactta ctattcaatt tcagctggta atgttggtat tcaatcttta 3000
588 gatgtgggat tccaagatgt tgttctaagt aaggttccta caattcccaa gtttagagat 3060
589 attactcaac attttattaa gaaaggagat gtgcctagag ccttgaatcg cttggcaaca 3120
590 ttagtgacaa ccgttaatgg aactcctatg ttaatttctg agggaccttt aaaaatggaa 3180
591 gaaaaagcca cttatgttca taagaagaat gatggtacta cggttgattt gactgtagat 3240
592 caggcatgga gaggaaaagg tgaaggtcct cctggaatgt gtggtggggc ctagtgtca 3300
593 tcaaatcagt ccatacaaaa tgcaattttg ggtattcatg ttgctggagg aaattcaatt 3360
594 ctgtggcaa agttgattac tcaagaaatg tttcaaaaaca ttgataagaa aattgaaatc 3420
595 aagctt 3426

```

598 <210> SEQ ID NO: 18

599 <211> LENGTH: 19

E--> 600 <212> TYPE: ADN

601 <213> ORGANISM: Chimeric Sequence

603 <220> FEATURE:

604 <221> NAME/KEY: sig_peptide

605 <222> LOCATION: (1)..(19)

606 <223> OTHER INFORMATION: Sequence #18.

607 Synthetic fragment corresponding to the

608 KDEL endoplasmic reticulum retention signal

609 sequence.

611 <400> SEQUENCE: 18

612 atcaaggatg aattgtaat

19

615 <210> SEQ ID NO: 19

616 <211> LENGTH: 21

E--> 617 <212> TYPE: ADN

618 <213> ORGANISM: Chimeric Sequence

620 <220> FEATURE:

621 <221> NAME/KEY: sig_peptide

622 <222> LOCATION: (1)..(21)

623 <223> OTHER INFORMATION: Sequence #19.

624 Synthetic fragment corresponding to the KDEL

625 endoplasmic reticulum retention signal sequence.

627 <400> SEQUENCE: 19

628 cgattacaat tcattccttga t

21

631 <210> SEQ ID NO: 20

RAW SEQUENCE LISTING

DATE: 07/11/2005

PATENT APPLICATION: US/10/540,615

TIME: 15:15:15

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\07112005\J540615.raw

520 gtcctatcaa cggactgaat catttgctct tcctcaatat ccatccc 47

523 <210> SEQ ID NO: 17

524 <211> LENGTH: 3426

E--> 525 <212> TYPE: ADN ← *Same error*

526 <213> ORGANISM: Hepatitis A virus

528 <220> FEATURE:

529 <221> NAME/KEY: gene

530 <222> LOCATION: Complement((1)..(3426))

531 <223> OTHER INFORMATION: Sequence # 17

532 Sequence coding for the modified open reading

533 frame (?ORFm) of the Cuban M2 strain of the HAV.

534 This sequence does not have the gene coding

W--> 535 for the VP4 protein.

537 <400> SEQUENCE: 17

538 gggatggata ttgaggaaga gcaaatgatt cagtcggttg ataggactgc agtgactgga 60

539 gcttcttatt tcacttctgt ggaccaatct tcagttcata ctgctgaggt tggctcacac 120

540 caaattgaac ctttgaaaac ctctgttgat aaacctggtt ctaagaaaac tcagggggag 180

541 aagtttttct tgattcattc tgctgattgg ctactacac atgctctctt tcatgaagtt 240

542 gcaaaattgg atgtggtgaa actgctgtac aatgagcagt ttgccgtcca aggtttgttg 300

543 agataccata cttatgcaag atttggcatt gagattcaag ttcagataaa tcccacaccc 360

544 tttcagcaag gaggactaat ctgtgccatg gttcctggtg accaaagtta tggttcaata 420

545 gcatccttga ctgtttatcc tcatggctg ttaaattgca atatcaacaa tgtagttaga 480

546 ataaagggtc catttattta tactagaggt gcttatcatt ttaaagatcc acagtacca 540

547 gtttgggaat tgacaatcag agtttgggtc gagttgaata ttggaacagg aacctcagct 600

548 tatacttcac tcaatgtttt agctaggttt acagatttgg agttgcatgg attaaactcct 660

549 ctttctacac agatgatgag aaatgaattt agagttagta ctactgaaaa tgttgtaaat 720

550 ttgtcaaatt atgaagatgc aagggcaaaa atgtcttttg ctttggatca ggaagattgg 780

551 aagtctgatc cttcccaagg tgggtggaatt aaaattactc atttcactac ctggacatcc 840

552 attccaacct tagctgctca gtttccattc aatgcttcag attcagttgg gcaacaaatt 900

553 aaagtataac cagtggagcc atacttttct cagatgacaa acactaatcc tgatcaaaaa 960

554 tgtataacag ccttggcctc tatttgtcag atgttctgct tttggagggg agatcttgtt 1020

555 ttcgatttcc aggtttttcc aaccaaatat cattcaggta ggctgttgtt ttgttttgtt 1080

556 cctgggaatg agttaataga tgttactgga attacattaa aacaggcaac tactgctcct 1140

557 tgtgcagtga tggacattac aggagtgcag tcaaccttga gatttcgtgt tccttggatt 1200

558 tctgatacac cctatcgagt gaataggtac acgaagtcag cacatcaaaa aggtgagtat 1260

559 actgccattg ggaagcttat tgtgtattgt tataatagat tgacttctcc ttctaagtgt 1320

560 gcttctcatg ttagagttaa tgtttatctt tcagcaatta atttggaatg ttttgctcct 1380

561 ctttaccatg ctatggatgt taccacacag gttggagatg attcaggagg tttctcaaca 1440

562 acagtttcta cagagcagaa tgttcctgat cccaagttg gcataacaac catgagggat 1500

563 ttaaaaggga aagccaatag gggaaaagat gatgtatcag gagtgcaggt acctgtggga 1560

564 gctattacaa caattgagga tccagtttta gcaaagaaag tacctgagac atttctgaa 1620

565 ttgaagcctg gagaatccag acatacatca gatcacatgt ctatttataa attcatggga 1680

566 aggtctcatt tcttgtgtac ttttactttt aattcaaaca ataaagagta cacatttcca 1740

567 ataactctgt cttcgacttc taatcctcct catggtttac catcaacatt aaggtggttc 1800

568 ttttaatttgt ttcagttgta tagaggacca ttggatttga caattataat cacaggagcc 1860

569 actgatgtgg atggtatggc ctggtttact ccagtgggcc ttgctgtcga cacccttgg 1920

570 gtggaaaaga agtcagcttt gtctattgat tataaaaactg cccttggagc tgttagattt 1980

571 aatacaagaa gaacagggaa cattcagatt agattgccat ggtattctta tttgtatgcc 2040

572 gtgtctggag cactggatgg cttgggagat aagacagatt ctacatttgg attggtttct 2100

RAW SEQUENCE LISTING

DATE: 07/11/2005

PATENT APPLICATION: US/10/540,615

TIME: 15:15:15

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\07112005\J540615.raw

```

462 tgggtggaaa agaagtcagc tttgtctatt gattataaaa ctgcccttgg agctgttaga 2040
463 ttttaatacaa gaagaacagg gaacattcag attagattgc catgggtattc ttatttgtat 2100
464 gccgtgtctg gagcactgga tggcttgagg gataagacag attctacatt tggattgggt 2160
465 tctattcaga ttgcaaatta caatcattct gatgaatatt tgtcctttag ttgttatttg 2220
466 tctgtcacag agcaatcaga gttctatttc cctagagctc cattaaattc aaatgctatg 2280
467 ttgtccactg agtccatgat gagtagaatt gcagctggag acttggagtc atcagtggat 2340
468 gatcccagat cagaggagga cagaagattt gagagtcata tagaatgtag gaaaccatat 2400
469 aaagaattga gactggagggt tgggaaacaa agaatcaaat atgctcagga agagttatca 2460
470 aatgaagtgc ttccacctcc taggaaaatg aaggggttat tttcacaagc tgaattcctg 2520
471 cagcccgggg gatccatggg aatttcagat gatgacaatg atagtgcagt agctgagttt 2580
472 ttccggtctt ttccatctgg tgaaccatca aattccaagt tatctagttt tttccaagct 2640
473 gtcactaatc acaagtgggt tgctgtggga gctgcagttg gtattcttgg attgctagtg 2700
474 ggaggatggt ttgtgtataa gcatttttcc cgcaaagagg aagaaccaat tccagctggt 2760
475 ggggtttatc atggagtgc taagcccaaa caagtgatta aattggatgc agatccagta 2820
476 gagtctcagt tgactctaga aatagcagga ttagttagga aaaatttggt tcagtttgga 2880
477 gttggtgaga aaaatggatg tgtgagatgg gtcatgaatg ccttaggagt gaaggatgat 2940
478 tggttgttag taccttctca tgcttataaa tttgaaaagg attatgaaat gatggagttt 3000
479 tatttcaata gaggtggaac ttactattca atttcagctg gtaatgttgt tattcaatct 3060
480 ttagatgtgg gattccaaga tgttgttcta atgaagttc ctacaattcc caagtttaga 3120
481 gatattactc aacattttat taagaaagga gatgtgccta gagccttgaa tcgcttgga 3180
482 acattagtga caaccgttaa tggaaactcct atgttaattt ctgagggacc tttaaaaatg 3240
483 gaagaaaaag ccacttatgt tcataagaag aatgatggta ctacggttga tttgactgta 3300
484 gatcaggcat ggagaggaaa aggtgaaggt cttcctggaa tgtgtggtgg ggccctagt 3360
485 tcatcaaatc agtccatata aaatgcaatt ttgggtattc atgttgctgg aggaaattca 3420
486 attcttgtgg caaagttgat tactcaagaa atgtttcaaa acattgataa gaaaattgaa 3480
487 atcaagctt 3489

```

```

490 <210> SEQ ID NO: 15
491 <211> LENGTH: 51
E--> 492 <212> TYPE: ADN
493 <213> ORGANISM: Chimeric Sequence
495 <220> FEATURE:
496 <221> NAME/KEY: gene
497 <222> LOCATION: (1)..(51)
498 <223> OTHER INFORMATION: Sequence # 15.
499     Synthetic fragment that reverts the
500     transcription start of the vp2 protein.
502 <400> SEQUENCE: 15
503 gggatggata ttgaggaaga gcaaatgatt cagtcctgtg ataggactgc a 51
506 <210> SEQ ID NO: 16
507 <211> LENGTH: 47
E--> 508 <212> TYPE: ADN
509 <213> ORGANISM: Chimeric Sequence
511 <220> FEATURE:
512 <221> NAME/KEY: gene
513 <222> LOCATION: (1)..(47)
514 <223> OTHER INFORMATION: Sequence # 16.
515     Synthetic fragment that reverts the transcription
516     start of the vp2 protein (complementary chain).
519 <400> SEQUENCE: 16

```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/540,615

DATE: 07/11/2005
TIME: 15:15:15

Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\07112005\J540615.raw

Same error

```

346 <210> SEQ ID NO: 11
347 <211> LENGTH: 25
E--> 348 <212> TYPE: ADN
349 <213> ORGANISM: Chimeric Sequence
351 <220> FEATURE:
352 <221> NAME/KEY: primer bind
353 <222> LOCATION: (1)..(25)
354 <223> OTHER INFORMATION: Sequence # 11.
355     Sequence of the oligonucleotide # 11 used
356     for the amplification of 3C coding sequence by PCR
359 <400> SEQUENCE: 11
360 tctcagtc aa ctctagaaat agcag
363 <210> SEQ ID NO: 12
364 <211> LENGTH: 21
E--> 365 <212> TYPE: ADN
366 <213> ORGANISM: Chimeric Sequence
368 <220> FEATURE:
369 <221> NAME/KEY: primer bind
370 <222> LOCATION: (1)..(21)
371 <223> OTHER INFORMATION: Sequence # 12.
372     Sequence of the oligonucleotide # 12 used for
373     the amplification of 3C coding sequence by PCR
376 <400> SEQUENCE: 12
377 ataagcttga tcaattttct t
380 <210> SEQ ID NO: 13
381 <211> LENGTH: 978
E--> 382 <212> TYPE: ADN
383 <213> ORGANISM: Hepatitis A virus
385 <220> FEATURE:
386 <221> NAME/KEY: gene
387 <222> LOCATION: Complement((1)..(978))
388 <223> OTHER INFORMATION: Sequence # 13.
389     Sequence corresponding to the region of 3ABC
390     polyprotein with proteolytic activity having
391     the selfprocessing sites mutated.
394 <400> SEQUENCE: 13
395 gaattcctgc agcccggggg atccatggga atttcagatg atgacaatga tagtgcagta 60
396 gctgagtttt tccggtcttt tccatctggt gaaccatcaa attccaagtt atctagtttt 120
397 ttccaagctg tcaactaatca caagtgggtt gctgtgggag ctgcagttgg tattcttgga 180
398 ttgctagtgg gaggatgggt tgtgtataag catttttccc gcaaagagga agaaccaatt 240
399 ccagctgttg gggtttatca tggagtgact aagcccaaac aagtgattaa attggatgca 300
400 gatccagtag agtctcagtt gactctagaa atagcaggat tagttaggaa aaatttggtt 360
401 cagtttgagg ttggtgagaa aaatggatgt gtgagatggg tcatgaatgc cttaggagtg 420
402 aaggatgatt gggtgttagt accttctcat gcttataaat ttgaaaagga ttatgaaatg 480
403 atggagtttt atttcaatag aggtggaact tactattcaa tttcagctgg taatgttggt 540
404 attcaatctt tagatgtggg attccaagat gttgttctaa tgaagggtcc tacaattccc 600
405 aagtttagag atattactca acattttatt aagaaaggag atgtgcctag agccttgaat 660
406 cgcttggcaa cattagtgac aaccgttaat ggaactccta tgtaatttc tgagggacct 720
407 ttaaaaaatgg aagaaaaagc cacttatgtt cataagaaga atgatggtac tacggttgat 780

```

RAW SEQUENCE LISTING

DATE: 07/11/2005

PATENT APPLICATION: US/10/540,615

TIME: 15:15:15

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\07112005\J540615.raw

```

408 ttgactgtag atcaggcatg gagaggaaaa ggtgaaggtc ttcctggaat gtgtggtggg 840
409 gccctagtgt catcaaatca gtccatacaa aatgcaattt tgggtattca tgttgctgga 900
410 ggaaattcaa ttcttggtggc aaagttgatt actcaagaaa tgtttcaaaa cattgataag 960
411 aaaattgaaa tcaagctt                                     978
414 <210> SEQ ID NO: 14
415 <211> LENGTH: 2489
E--> 416 <212> TYPE: ADN same error
417 <213> ORGANISM: Hepatitis A virus
419 <220> FEATURE:
420 <221> NAME/KEY: gene
421 <222> LOCATION: Complement((1)..(3489))
422 <223> OTHER INFORMATION: Sequence # 14.
423     Nucleotide sequence CODING for the new
424     modified open reading frame (ORFm) of the
425     Cuban M2 strain.
428 <400> SEQUENCE: 14
429 atgaatatgt ccaaacaaagg aattttccag actgttggga gtggccttga ccacatcctg 60
430 tccttggcag atattgagga agagcaaagt attcagtcctg ttgataggac tgcagtgact 120
431 ggagcttctt atttcacttc tgtggaccaa tcttcagttc atactgctga ggttggctca 180
432 caccaaattg aacctttgaa aacctctggt gataaacctg gttctaagaa aactcagggg 240
433 gagaagtttt tcttgattca ttctgctgat tggctcacta cacatgctct ctttcatgaa 300
434 gttgcaaaat tggatgtggt gaaactgctg tacaatgagc agtttgccgt ccaaggtttg 360
435 ttgagatacc atacttatgc aagatttggc attgagattc aagttcagat aaatcccaca 420
436 ccctttcagc aaggaggact aatctgtgcc atggttcctg gtgaccaaag ttatggttca 480
437 atagcatcct tgactgttta tcctcatggt ctgttaaatt gcaatatcaa caatgtagtt 540
438 agaataaaag ttccatttat ttatactaga ggtgcttatt attttaaaga tccacagtac 600
439 ccagtttggg aattgacaat cagagtttgg tcagagttga atattggaac aggaacctca 660
440 gcttatactt cactcaatgt tttagctagg tttacagatt tggagttgca tggattaact 720
441 cctctttcta cacagatgat gagaaatgaa tttagagtta gtactactga aaatgttgta 780
442 aatttgtaaa attatgaaga tgcaagggca aaaatgtctt ttgctttgga tcaggaagat 840
443 tgggaagtctg atccttccca aggtggtgga attaaaatta ctcatttcac tacctggaca 900
444 tccattccaa ccttagctgc tcagtttcca ttcaatgctt cagattcagt tgggcaacaa 960
445 attaaaagta taccagtgga cccatacttt ttccagatga caaacactaa tctgatcaa 1020
446 aaatgtataa cagccttggc ctctatttgt cagatgttct gcttttggag gggagatctt 1080
447 gttttcgatt tccaggtttt tccaaccaa tatcattcag gtaggctgtt gttttgtttt 1140
448 gttcctggga atgagttaat agatgttact ggaattacat taaaacaggc aactactgct 1200
449 ccttggtgag tgatggacat tacaggagtg cagtcaacct tgagatttcg tgttccttgg 1260
450 atttctgata caccctatcg agtgaatagg tacacgaagt cagcacatca aaaaggtgag 1320
451 tatactgcc a ttgggaagct tattgtgtat tggtataata gattgacttc tccttctaatt 1380
452 gttgcttctc atgttagagt taatgtttat ctttcagcaa ttaatttga atgttttgct 1440
453 cctctttacc atgctatgga tgttaccaca caggttggag atgattcagg aggtttctca 1500
454 acaacagttt ctacagagca gaatgttctt gatccccaag ttggcataac aacctagagg 1560
455 gatttaaaaag ggaaaagcaa taggggaaag atggatgtat caggagtgca ggtacctgtg 1620
456 ggagctatta caacaattga ggatccagtt ttagcaaaga aagtacctga gacatttcct 1680
457 gaattgaagc ctggagaatc cagacataca tcagatcaca tgtctattta taaattcatg 1740
458 ggaaggtctc atttctgtg tacttttact ttttaattcaa acaataaaga gtacacattt 1800
459 ccaataactc tgtcttcgac ttctaactct cctcatggtt taccatcaac attaaggtgg 1860
460 ttctttaatt tgtttcagtt gtatagagga ccattggatt tgacaattat aatcacagga 1920
461 gccactgatg tggatggtat ggcctggttt actccagtgg gccttgctgt cgacaccctt 1980

```

RAW SEQUENCE LISTING

DATE: 07/11/2005

PATENT APPLICATION: US/10/540,615

TIME: 15:15:15

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\07112005\J540615.raw

275 <213> ORGANISM: Chimeric Sequence ← Same error.

277 <220> FEATURE:

278 <221> NAME/KEY: primer_bind

279 <222> LOCATION: (1)..(27)

280 <223> OTHER INFORMATION: Sequence # 7.

281 Sequence of the oligonucleotide # 7 used for

282 the amplification of 3A coding sequence by PCR.

285 <400> SEQUENCE: 7

286 ccatgggaat ttcagatgat gacaatg 27

289 <210> SEQ ID NO: 8

290 <211> LENGTH: 26

E--> 291 <212> TYPE: ADN ← Same error

292 <213> ORGANISM: Chimeric Sequence

294 <220> FEATURE:

295 <221> NAME/KEY: primer_bind

296 <222> LOCATION: (1)..(26)

297 <223> OTHER INFORMATION: Sequence # 8.

298 Sequence of the oligonucleotide # 7 used for

299 the amplification of 3A coding sequence by PCR.

302 <400> SEQUENCE: 8

303 ggatatcggt tcttctcttt tgcggg 26

306 <210> SEQ ID NO: 9

307 <211> LENGTH: 85 ← Same error

E--> 308 <212> TYPE: ADN

309 <213> ORGANISM: Chimeric Sequence

312 <220> FEATURE:

313 <221> NAME/KEY: gene

314 <222> LOCATION: (1)..(85)

315 <223> OTHER INFORMATION: Sequence # 9.

316 Synthetic fragment coding for 3B protein

317 carrying T by C and G by C nucleotide

318 substitutions, respectively.

321 <400> SEQUENCE: 9

322 tccagctggt ggggtttatc atggagtgac taagcccaaa caagtgatta aattggatgc 60

323 agatccagta gagtctcagt tgact 85

326 <210> SEQ ID NO: 10

327 <211> LENGTH: 89 ← Same error

E--> 328 <212> TYPE: ADN

329 <213> ORGANISM: Chimeric Sequence

332 <220> FEATURE:

333 <221> NAME/KEY: gene

334 <222> LOCATION: (1)..(89)

335 <223> OTHER INFORMATION: Sequence # 10.

336 Synthetic fragment coding for 3B protein

337 carrying T by C and G by C nucleotide

338 substitutions, respectively (complementary chain).

341 <400> SEQUENCE: 10

342 ctagagtcaa ctgagactct actggatctg catccaattt aatcacttgt ttgggcttag 60

343 tcaactccatg ataaacccca acagctgga 89